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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patients with peanut hypersensitivity.";
J. Clin. Invest. 96:1715-1721(1995).
-!- SIMILARITY: TO 7S SEED STORAGE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arachis hypogaea (Peanut).
Eukaryota; Viridiplantae; Embryophy
Magnoliophyta; eudicotyledons; core
Fabales; Fabaceae; Papilionoideae;
          protein
                     alpha, alpha'
                               Schuler M.A., "Structural se
                                                     MEDLINE-83143289;
                                                                                         "The glycosylated seed vulgaris. Structural ho
                                                                                                                                                                         Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. FLORUNNER; MEDLINE=96013631; PubMed=7560062;
  Nucleic
                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
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  Acids
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                                                                                  Chem.
                                                                                                                                                                Fabaceae;
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                                                                                 Structural homologies of Chem. 261:9228-9238(1986).
                                                                                                                                                                                                                                                                                                                  97
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                               1., Ladin B.
sequences
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Swiss Institute of Bioinformatics
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                                         Ladin
                       and
                639 FROM N.A.

9; PubMed=6897678;

adin B.F., Pollaco J.C.
nuences are conserved i
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                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                 PubMed=3013879;
                                                                                                                                                                Papilionoideae;
                                                                                                                       M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               71345 MW;
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                                                                                                    storage proteins
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                                                                                                                         Godette
                                                                                                                                                                                 Embryophyta; Tracheophyta; Spermatophyta;
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                    the genes soybean 7s
                         , Freyer G., beau...
                                                                                                    of Glycine max
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sion and IgE )
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Best Local :
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P13916;
01-JAN-1990
01-APR-1990
15-DEC-1998
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CARBOHYD
CONFLICT
CONFLICT
CONFLICT
                                                            Plant
-!- FU
                                                                                            "Complete sequence of a cDNA of alpha conglycinin.";
                                                                                                                                                                                                                                                       Glycine max (Soybean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-APR-1990 (Rel. 14, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
BETA CONGLYCININ, ALPHA CHAIN PRECURSO
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J01290; -; NOT
PIR; B24810; B24810.
HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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EMBL; J01290; -; NOT_ANNO
                                                                                                                                                         TISSUE=COTYLEDON;
MEDLINE=91355860;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                         Fabales;
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                  nt Mol. Biol. 15:197-201(1990).
FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HUDROLYZED AFTER GERMINATION TO PROVIDE CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING. SUBUNIT: THE ALPHA', ALPHA', AND BETA-SUBUNITS ASSOCIATE VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY:
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ALPHA'-,
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                                                                                                                                                           PubMed=2103438;
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30.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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Pred. No. 0.00
10; Mismatches
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N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

P -> L (IN REF. 2).

M -> V (IN REF. 2).

S -> T (IN REF. 2).
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AND
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subunit
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BETA-SUBUNITS
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RESULT 5
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Best Local s
Matches 22
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Woessner
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CARBOHYD
SEQUENCE
SEQUENCE OF 39-182 FROM N.A.

ROHLFING T., Tin-Wollam A.M., Duckels G.;

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES BY A MOTILITY-INHIBITING MECHANISM. BINDS TO THE COMPLEX NEUROPILIN-1/PLEXIN-1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Cr
30-MAY-2000 (Rel. 39, La
30-MAY-2000 (Rel. 39, La
SEMAPHORIN 3A PRECURSOR
                                                                                                                                                                                                                                                                                                                                          Kolodkin A.L., Matthes D.J., Goodman (
"The semaphorin genes encode a family growth cone guidance molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM3A_HUMAN
Q14563;
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Seed storage protein; Signal;
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                                                                                                                                                                                                              Woessner J., Minx P., H.
Submitted (MAR-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=FETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VACUOLAR PROTEIN BODIES
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22; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FWSYBA.
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EMBL/GenBank/DDBJ
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                   This SWI
between
                                                                                                                                              Chlan C.A., Borroto K., Kamalay J.A., Dure L. III; "Developmental biochemistry of cottonseed embryogenesis germination. XIX. Sequences and genomic organization of globulin (vicilin) genes of cottonseed."; Plant Mol. Biol. 9:533-446(1987).
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN
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DOMAIN: STRONG BINDING
THIRD OF THE PROTEIN.
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 Swiss Institute
Bioinformatics
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                                                                                                                                                                                                                                                            N.A.
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                                                                                                                               LOCATION:
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                                    is copyright.
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ARG/LYS-RICH (BASIC).
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                   jht. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
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ion update)
DBULIN A).
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                                                                                          VICILIN,
               outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (EC
                                                EMBL; J05047; AAA37044.1;
PIR; A36502; A36502.
HSSP; P06213; 1IRK.
                                                                                          entities requires a or send an email to
                                                                                                                            between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=89359245; Pu Shier P., Watt V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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PFAM; PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                       ENTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                          "Primary structure of a putative receptor for a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 CEQSCREQYEKQQQQQPD---KQFKECQQRCQWQEQRPERKQQCVKECREQYQEDPWKGER 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 CLQSC------QQEPDDLKQ-KACESRCTKLEYDP----RCYYDTGATNQRHP-PGER
                                                                                                                                                                                                                                                                     BIOL. Chem. 264:14605-14608(1989).

FUNCTION: THIS RECEPTOR PROBABLY BINDS AN INSULIN RELATED AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PROSPHATE.

SUBUNIT: PROBABLE TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LIDISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMAT THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE CHAINS DISULFIDE BONDS.
                                                                                                                                                                                                                                    SUBCELLULAR
SIMILARITY:
                                                                                                                                                                                                         SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                       PROTEIN KINASES
                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           storage protein;
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; IPR000494;
; IPR000719;
; IPR001245;
; IPR001777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
605 AA;
                                                                                                 equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Eut
Hystricognathi; Caviidae;
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                                                                                                                                        There are no restrictions ng as its content is in
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                                                                                                                             Usage
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DOMAIN
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BINDING
ACT_SITE
   SEQUENCE FROM N.A.

Chian C.A., Pyle J.B., Legocki A.B., Dure
"Developmental biochemistry of cottonseed
"Developmental biochemistry of cottonseed
                                                                                                                                                                              GOSHI STANDARD; PRT; 588 AA.

POLB_GOSHI STANDARD; PRT; 588 AA.

POSHO1;

O1-MAR-1989 (Rel. 10, Created)

O1-MAR-1989 (Rel. 10, Last sequence update)

O1-MAR-1999 (Rel. 38, Last annotation update)

VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).

GOSSYPIum hirsutum (Upland cortion).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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SEQUENCE
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PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS00239; RECEPTOR_TO.; 1.

PROSITE; PS050011; PROTEIN_KINASE_DOM; 1.

Olycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
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                                                                                                                                                      Malvales;
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INTERPRO; IPRO02174; -.
PFAM; PF00757; Furin-like;
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19; Conserv
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                                                                                                                                                         Malvaceae;
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31.1%;
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INSULIN RECEPTOR-RELATED
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Best Local Similarity
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97470885; PubMed=9331345;
Taniguchi M., Yuasa S., Fujisawa
                                                                                                                                                                                    Neuron
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                        008665; 062180; 062215;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the storage protein families.";
Plant Mol. Biol. 7:475-489(1986).
-:- FUNCTION: SEED STORAGE PROTEIN.
-:- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN BODIES.
-:- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
 TISSUE=FETAL BRAII MEDLINE=95267432;
                                                                                                                                                                                                     Pueschel A.W., Adams R.H., Betz H.;
"Murine semaphorin D/collapsin is a member of a dive
and creates domains inhibitory for axonal extension.
Neuron 14:941-948(1995).
                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                  SEQUENCE OF 107-772 FROM
                                                                  peripheral nerve project
Neuron 19:519-530(1997).
                                                                                                 "Disruption
                                                                                                                                                                                                                                                                    MEDLINE=95267431; PubMed=7748561;
                                                                                                                                                                                                                                                                                         STRAIN-NMRI;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         SEMAJA OR SEMAD OR
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tute of Bioinformatics
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Sciurognathi;
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 SEMAPHORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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EMBL; D85028; BAA19773.1;
EMBL; L40484; AAA73934.1;
MGD; MGI:107558; SEMA3A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Developmental
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SUBCELLULAR LOCATION: SECRETED.
BYVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYONIC DEVELOPMENT (E11) IN DISTINCT REGIONS OF THE NEUROECTODERM AND MESODERM.
EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SEMAPHURIN FRANCE.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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                                                                                                                                                                                                                            l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Multigene family; Neurogenesis;
mental protein; Glycoprotein.
0 (Rel. 39, Created)
0 (Rel. 39, Last sequence up
0 (Rel. 39, Last annotation
3A PRECURSOR (SEMAPHORIN II
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N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
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D-> G (IN REF. 1)
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OH-> ED (IN REF. 1)
OH-> ED (IN REF. 1)
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Pred. No. 7.5;
6; Mismatches
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(III
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Matches 18
UL49_EBV
P14347;
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CARBOHYD
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SEQUENCE
                                                  _EBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97073089; PubMed=8915837; Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.; Giger R.J. wolfer D.P., De Wit G.M.J., Verhaagen J.; "Anatomy of rat seemaphorin III/Collapsin-1 mRNA expression and relationship to developing nerve tracts during neuroembryogenesis."; J. Comp. Neurol. 375:378-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. use by non-profit institutions as low modified and this statement is not remove
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SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE OLFACTORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC VESICLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND SONITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESENCHYMAL LEVELS DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC SETS OF NEURONS IN THE CNS. IN THE MATURE CNS, IT IS DETECTABLE IN MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORTEX, CEREBELLAR PURKINGE CELLS, AS WELL AS A SUBSET OF CRANIAL AND CEREBELLAR PURKINGE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS ENGAGE IN THE FORMATION OF SPECIFIC NERVE TRACTS. BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN:
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                                                                                                          AQLPLHRC - - -
                                                                                                                                     AQRCLQSCQQEPDDLKQKACESRCTKLEYDPRCVYDTGATNQRHPPGERTRGRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X95286; CAA64607.1;
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                                                                                                                                                                   18; Conservative
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Dta; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001627;
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                                                                                                                                                                                                                                   1 protein; (1) 20 21 772 40 538 43 770 0 723 3 53 125 591
                                STANDARD;
                                                                                                          -DIYGKACAECC--LARDPYCAWDGSSCSRYFPTAKRRTRRQ
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          institutions as long as its content is in no way tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                 18.5%;
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Glycoprotein.
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                                                                                                                                                                   ; Score 63.5; D; Pred. No. 7.5; 6; Mismatches
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
240907812FF9F2D2 CRC64;
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01-JUL-1993
01-NOV-1995
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                                   -i- PATHWAY: BRANCH-POINT REACTIONS BETWEEN GEN
METABOLISM AND PATHWAYS LEADING TO VARIOUS
-i- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA
COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                    J. Biol. Chem. 266:8551-8559(1991).
-!- CATALYTIC ACTIVITY: ATP + 4-COUMARATE + COA =
                                                                                                                                                                                                                                                                                                                              4CL1_SOLTU
P31684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epstein-barr virus (strain B95-8) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Cammaherpesvirinae; Lymphocryptovirus.
            This SWISS-PROT
                                                                                                                           "Structural comparison, modes of expression, and pelements of the two 4-commarate: CoA ligase genes
                                                                                                                                                        Becker-Andre M., Schulze-Lefert P., Hahlbrock K.;
                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=91217100;
                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Trache
Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                               Solanum tuberosum (Potato).
                                                                                                                                                                                                                                                               4CL-1.
                                                                                                                                                                                                                                                                            4 - COUMARATE
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SEQUENCE 59
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HVS-1 66, AND HCMV UL49.
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, Bankier A.T., Bio
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                                                                                                                                                                                                            Solanaceae;
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(Rel. 26, Last sequence update)
(Rel. 32, Last annotation update)
--COA LIGASE 1 (EC 6.2.1.12) (4CL)
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A.T., Biggin M.D., Double G., Hudson G.S.,
                                                                                                                                                                      PubMed=2022667;
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                                                              BETWEEN GENERAL PHENYLPROPANOID TO VARIOUS SPECIFIC END PRODUCTS
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01-JUL-1993
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 SM3D_HUMAN 095025;
                                                                                                                                                                                                                                                                                                         COVALENT BINDING OF AMP TO THEIR SUBSTRATE PIR; B39827; B39827.
HSSP; P08659; ILCI.
                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural comparison, modes of expression, and putative cis-acting elements of the two 4-coumarate: CoA ligase genes in potato.";
J. Biol. Chem. 266:8551-8559(191).
-i- CATALTIC ACTIVITY: ATP + 4-COUMARATE + COA = AMP + PYROPHOSPHATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embr
Magnoliophyta; eudicotyledons;
Solanales; Solanaceae; Solanum
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PROSITE; PS00455; AMP_BINDING; 1.
Ligase; Phenylpropanoid metabolism; Multigene family.
SEQUENCE 545 AA; 59625 MW; 5481F0BOAFEA39EO CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91217100; PubMed=2022667;
Becker-Andre M., Schulze-Lefert P., Hahlbrock K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING; 1.
Ligase; Phenylpropanoid metabolism; Multigene family.
SEQUENCE 545 AA; 59619 MW; DE183683B774BA71 CRC64;
                                                                                                                                                                                                                                                                                              INTERPRO;
                                                                                                                                                                                                                                                                                                                                                      -i- PATHWAY: BRANCH-POINT REACTIONS BETWEEN GENERAL PHENYLPROPANOID METABOLISM AND PATHWAYS LEADING TO VARIOUS SPECIFIC END PRODUCTS -i- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solanum tuberosum (Potato).
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HSSP; P08659; 1LCI.
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                                                                                                                       4 PCAQRCLQSCQQEPDDLKQKACESRCTKLE---YDPRCVYDTGATNQRHPPGE 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European
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                                                                                                                                                      l Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                            IPR000873; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 32, Last annotation update)
--COA LIGASE 2 (EC 6.2.1.12) (4CL)
                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                    17.8%;
35.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta; Spermatophyta;
dons; core eudicots; Asteridae; euasterids I;
                                                                                                                                                      Score 61; DB Pred. No. 10; 6; Mismatches
                                                                                                                                                      6;
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Pred. No. 10;
                PRT;
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RESULT 15
PGBM_HUMAL
ID PGBM_H
AC P98160
DT 01-OCT
DT 01-OCT
DT 15-JUL
DE BASEME
DE PROTEEL
GN HSPG2.
OS HOMO S
OC EUKARY
OC Mammal
RN [1]
RP SEQUEN
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Matches
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CARBOHYD
SEQUENCE
                                                                                                                                                        PGBM_HUMAN STANDARD; PRT; 4393 AA.

P98160; 016287;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DISULFID
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PFAM; PF00047; ig; l.
PFAM; PF00047; ig; l.
Cianal; Immunoglobulin domain; Multi-
Cianal; Immunoglobulin domain; Multi-
Potenti; Glycoprotein.
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30-MAY-2000
30-MAY-2000
                                              Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mead K., Graves T., Wilson C. Submitted (JUN-1998) to the E
    SEQUENCE FROM N.A
                                                                                                                                         PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                         528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 QRCLQSCQQEPDDLKQKACESRCTKLEYDPRCVYDTGATNQRHPPGERTRGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. FUNCTION: INDUCES THE COLLARSE AND PARALYSIS OF NEURONAL GROWTH CONES. COULD POTENTIALLY ACT AS REPULSIVE CUES TOWARD SPECIFIC NEURONAL POPULATIONS. BINDS TO NEUROPILIN (BY SIMILARITY). SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE THIRD OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                         QLSLHRC----DTYGKACADCC--LARDPYCAWDGNACSRYAPTSKRRARRQ 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001627;
; IPR001899;
; IPR003006;
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Metazoa; Chordata; C
~··heria; Primates; (
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89651 MW;
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39, Last:
39, Last:
                                              Chordata;
Primates;
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ARG/LYS-RICH (BASIC).
BY SIMILARITY.
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N-LINKED (GLCNAC...) (PO'
N-LINKED (GLCNAC...) (PO'
N-LINKED (GLCNAC...) (PO'
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60.5;
Pred. No. 16;
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                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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This
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SUBUNIT: PUBLIFIED PERLECAN HAS A STRONG TENDENCY TO AGGREGATE 1
DIMERS OR STELLATE STRUCTURES.

SUBCELLULAR LOCATION: EXTRACELLULAR.

SUBCELLULAR LOCATION: EXTRACELLULAR.

FTM: CONTAINS THERE HEDARAN SULFATE CHAINS AS WELL AS N-LINKED DIAGOSACCHARIDES.

SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
SIMILARITY: CONTAINS 3 LAMININ G-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics [5]
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[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   basement membrane (HSPG2/perlecan). A chimeric molecule with multiple domains homologous to the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor.";

J. Biol. Chem. 267:8544-8557(1992).
                                           entities re
or send an
                                                                        modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-21 FROM N.A.
MEDLINE-94052171; PubMed-8234307;
MEDHONE-94052171; PubMed-8234307;
Cohen I.R., Graessel S., Murdoch A.D., Iozzo
"Structural characterization of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=CULON;
MEDLINE=91365376; PubMed=1679749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=SKIN, AND COLON;
MEDLINE=92235084; PubMed=1569102;
Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., I
"Primary structure of the human heparan sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human
467-kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1018-1472 FROM N.A. TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   its promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assignment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tryggvason K
"Cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kallunki P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92120660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92112994; PubMed=1730768;
Kallunki P., Tryggvason K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BamHI restriction fragment length anomics 11:389-396(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uman basement membrane heparan sulfate proteoglycan core protein: a '-kD protein containing multiple domains resembling elements of the w density lipoprotein receptor, laminin, neural cell adhesion lecules, and epidermal growth factor."; Cell Biol. 116:559-571(1992).
                                                                                                      ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                        C. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).

EUNCTION: THIS PROTEIN IS AN INTECRAL COMPONENT OF BASEMENT
MEMBRANES. IT IS RESPONSIBLE FOR THE FIXED NEGATIVE ELECTROSTATIC
CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILTRATION
PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS
SUCH AS LAMININ AND COLLAGEN TYPE IV AND SERVES AS AN ATTACHMENT
                                                                                                                  SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the Ex
х62515;
м85289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arm of
                                         non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n of human chromosome 10:673-680(1991).
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Eddy R.L., Byers M.G.,
CAA44373.1;
AAA52700.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene (HSPG2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sulfate proteoglycan core protein,
SPG2) to 1p36.1-->p35 and identification
ent length polymorphism.";
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1.";
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                                                                                                      There are no
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                                                                                                      restrictions
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                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                  a collaboration
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                                                                                                                      ontstation
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                                                                                                      on
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PEAM; PRO0054; Laminin_G; 3.

PEAM; PE00057; ldl_recept_a; 4.

PRINTS; PR00010; EGFBLOOD.

PROSITE; PS00022; EGF_1; 9.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01248; LAMININ_TYPE_EGF; 1.

PROSITE; PS50068; LDLRA_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00008;
PEAM; PF001390;
PFAM; PF000547;
PFAM; PF00053;
PFAM; PF00054;
PFAM; PF00054;
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MTM; 142461;
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laminin_G; 3.
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EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN II (4 LDLRA REPEATS).

DOMAIN II A (1 IGG-REPEAT).

DOMAIN III (SIMILAR TO SHORT ARM OF LAMININ A CHAIN).

DOMAIN IV (SIMILAR TO NEURAL CELL ADHESION MOLECULE; 21 IGG REPFATTS).
ALPHA CHAINS AND EGP)

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LAMININ EGF-LIKE 1 (C-TER LAMININ EGF-LIKE 1 (C-TER LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 5 (C-TER LAMININ EGF-LIKE 5 (C-TER LAMININ EGF-LIKE 5 (C-TER LAMININ EGF-LIKE 5 (C-TER LAMININ EGF-LIKE 9 (N-TER LAMININ EGF-LIKE 9 (N-TER LAMININ EGF-LIKE 9 (C-TER LAMININ EGF-LIKE 9 (C-TER LAMININ EGF-LIKE 9 (C-TER LAMININ EGF-LIKE 9 (C-TER LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

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IN EGF-LIKE 1 (N-TERMINAL).
IN LOMAIN IV 1 (DOMAIN III A).
IN EGF-LIKE 1 (C-TERMINAL).
IN EGF-LIKE 2
IN EGF-LIKE 4 (INCOMPLETE).
IN EGF-LIKE 5 (N-TERMINAL).
IN EGF-LIKE 5 (N-TERMINAL).
IN LOMAIN IV 2 (DOMAIN III B).
IN EGF-LIKE 6.
IN EGF-LIKE 7.
IN EGF-LIKE 8.
IN EGF-LIKE 9 (N-TERMINAL).
IN EGF-LIKE 9 (N-TERMINAL).
IN EGF-LIKE 9 (N-TERMINAL).
IN EGF-LIKE 10.
IN EGF-LIKE 11.
IN EGF-LIKE 10.
IN EGF-LIKE 5 (C-TERMINAL).
IN EGF-LIKE 10.
IN EGF-LIKE 5 (C-TERMINAL).
IN EGF-LIKE 5 (C-TERMINAL).
IN EGF-LIKE 10.
IN EGF-LIKE 5 (C-TERMINAL).
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IN EGF-LIKE 10.
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IN EGF-LIKE 5
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Best Local Similarity 32.2%;
Matches 19; Conservative
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                                            PCAQRCLQSCQQEPDDLKQKACESRCTKLEYDPRCVYDTGATN--QRHPPGERTRGRQP 60
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IG-LIKE C2-TYPE DOMAIN 12.
IG-LIKE C2-TYPE DOMAIN 13.
IG-LIKE C2-TYPE DOMAIN 14.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 17.
IG-LIKE C2-TYPE DOMAIN 19.
IG-LIKE C2-TYPE DOMAIN 20.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 21.
IG-LIKE C2-TYPE DOMAIN 22.
LAMININ G-LIKE 1 (GLOBULAR DOMAIN VERF-LIKE 2.
LAMININ G-LIKE 3.
EGF-LIKE 4.
LAMININ G-LIKE 3 (GLOBULAR DOMAIN VERF-LIKE 3.
EGF-LIKE 4.
LAMININ G-LIKE 3 (GLOBULAR DOMAIN VERF-LIKE 3.
EGF-LIKE 4.
LAMININ G-LIKE 3 (GLOBULAR DOMAIN VERF-LIKE 4.
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